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DATE: Thursday, March 03, 2005

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☐	L3	L2 same (size or length)	349
☐	L2	L1 same site	416
☐	L1	restriction fragment same sequence same (computer or program)	931

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                   alerts (SDIs) affected
 NEWS  11 DEC 17   SOLIDSTATE reloaded; updating to resume; current-awareness
                   alerts (SDIs) affected
 NEWS  12 DEC 17   CERAB reloaded; updating to resume; current-awareness
                   alerts (SDIs) affected
 NEWS  13 DEC 17   THREE NEW FIELDS ADDED TO IFIPAT/IFIUDB/IFICDB
 NEWS  14 DEC 30   EPFULL: New patent full text database to be available on STN
 NEWS  15 DEC 30   CAPLUS - PATENT COVERAGE EXPANDED
 NEWS  16 JAN 03   No connect-hour charges in EPFULL during January and
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 NEWS  17 FEB 25   CA/CAPLUS - Russian Agency for Patents and Trademarks
                   (ROSPATENT) added to list of core patent offices covered
 NEWS  18 FEB 10   STN Patent Forums to be held in March 2005
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                   National Meeting on March 13, 2005
 NEWS  20 FEB 28   PATDPAFULL - New display fields provide for legal status
                   data from INPADOC
 NEWS  21 FEB 28   BABS - Current-awareness alerts (SDIs) available
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FILE 'HOME' ENTERED AT 10:07:31 ON 03 MAR 2005

=> file .pub
COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION
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FILE 'MEDLINE' ENTERED AT 10:07:39 ON 03 MAR 2005

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=> s restriction fragment and sequence and site and (computer or program)
L1 202 RESTRICTION FRAGMENT AND SEQUENCE AND SITE AND (COMPUTER OR PROGRAM)

=> s l1 and (size or length)
L2 137 L1 AND (SIZE OR LENGTH)

=> d 1-10 bib ab

L2 ANSWER 1 OF 137 MEDLINE on STN
AN 2004531454 MEDLINE
DN PubMed ID: 15500921
TI Shotgun optical mapping of the entire Leishmania major Friedlin genome.
AU Zhou Shiguo; Kile Andrew; Kvikstad Erika; Bechner Mike; Severin Jessica; Forrest Dan; Runnheim Rod; Churas Chris; Anantharaman Thomas S; Myler Peter; Vogt Christy; Ivens Al; Stuart Kenneth; Schwartz David C
CS Laboratory for Molecular and Computational Genomics, UW Biotechnology Center, University of Wisconsin-Madison, 425 Henry Mall, Madison, WI 53706, USA.
SO Molecular and biochemical parasitology, (2004 Nov) 138 (1) 97-106. Journal code: 8006324. ISSN: 0166-6851.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200502
ED Entered STN: 20041026
Last Updated on STN: 20050211
Entered Medline: 20050210
AB Leishmania is a group of protozoan parasites which causes a broad spectrum of diseases resulting in widespread human suffering and death, as well as economic loss from the infection of some domestic animals and wildlife. To further understand the fundamental genomic architecture of this parasite, and to accelerate the on-going sequencing project, a whole-genome XbaI restriction map was constructed using the optical mapping system. This map supplemented traditional physical maps that were generated by fingerprinting and hybridization of cosmid and P1 clone libraries. Thirty-six optical map contigs were constructed for the corresponding known 36 chromosomes of the Leishmania major Friedlin genome. The chromosome **sizes** ranged from 326.9 to 2821.3 kb, with a total genome **size** of 34.7 Mb; the average XbaI **restriction fragment** was 25.3 kb, and ranged from 15.7 to 77.8 kb on a per chromosomes basis. Comparison between the optical maps and the in silico maps of **sequence** drawn from completed, nearly finished, or large **sequence** contigs showed that optical

maps served several useful functions within the path to create finished **sequence** by: guiding aspects of the **sequence** assembly, identifying misassemblies, detection of cosmid or PAC clones misplacements to chromosomes, and validation of **sequence** stemming from varying degrees of finishing. Our results also showed the potential use of optical maps as a means to detect and characterize map segmental duplication within genomes.

L2 ANSWER 2 OF 137 MEDLINE on STN
AN 2004314094 MEDLINE
DN PubMed ID: 15215682
TI The putative recombination of hepatitis B virus genotype B with pre-C/C region of genotype C.
AU Luo Kangxian; Liu Zhihua; He Haitang; Peng Jie; Liang Weifang; Dai Wei; Hou Jinlin
CS Department of Infectious Diseases, Nanfang Hospital, Guangzhou 510515, China.. heplab@fimmu.edu.cn
SO Virus genes, (2004 Aug) 29 (1) 31-41.
Journal code: 8803967. ISSN: 0920-8569.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AY217355; GENBANK-AY217356; GENBANK-AY217357; GENBANK-AY217358; GENBANK-AY217359; GENBANK-AY217360; GENBANK-AY217361; GENBANK-AY217362; GENBANK-AY217363; GENBANK-AY217364; GENBANK-AY217365; GENBANK-AY217366; GENBANK-AY217367; GENBANK-AY217368; GENBANK-AY217369; GENBANK-AY217370; GENBANK-AY217371; GENBANK-AY217372; GENBANK-AY217373; GENBANK-AY217374; GENBANK-AY217375; GENBANK-AY217376; GENBANK-AY217377; GENBANK-AY217378
EM 200410
ED Entered STN: 20040625
Last Updated on STN: 20041022
Entered Medline: 20041021
AB Among hepatitis B virus (HBV) genotypes the B and C are most prevalent in China. To further study on the inside story of the intertypes, the genotype of 136 **sequences** from Chinese patients were analyzed either by **restriction fragment length** polymorphism on fragments or by phylogenetic analysis and bootscanning on full genome. The 22 complete **sequences** of genotype B clustered with different genotypes depending on gene fragments analyzed, which indicated that recombinant events occurred during HBV evolutionary history. To locate the recombinant regions, the **sequences** of HBV entire genome were analyzed by SimPlot **program**. The recombinant regions of B genotype with recombination were mapped in the pre-C/C region with relatively less varied **size**. Besides, three **sequences** of genotype C have recombination with genotype B or D in different regions. However, among all of the 136 **sequences**, none of authentic genotype B was identified. To investigate the possible mechanism responsible for intertype recombination, the selection pressure on the recombinant region was estimated by using CODEML **program**. All models allow for positively selected **sites** suggest existence of positive selection pressure. In conclusion, the genotype B with recombination was exclusive subgroup of genotype B in China. The mosaic genotype B might result from immune pressure on the pre-C/C gene.

L2 ANSWER 3 OF 137 MEDLINE on STN
AN 2004140164 MEDLINE
DN PubMed ID: 14752001
TI In silico analysis of complete bacterial genomes: PCR, AFLP-PCR and endonuclease restriction.
AU Bikandi Joseba; San Millan Rosario; Rementeria Aitor; Garaizar Javier
CS Department of Immunology, Microbiology and Parasitology, University of the Basque Country, Paseo de la Universidad, 7, 01006 Vitoria-Gasteiz, Spain.. oipbibij@lg.ehu.es

SO Bioinformatics (Oxford, England), (2004 Mar 22) 20 (5) 798-9. Electronic Publication: 2004-01-29.
Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200411
ED Entered STN: 20040323
Last Updated on STN: 20041103
Entered Medline: 20041102
AB We have developed a website, www.in-silico.com, which runs a software **program** that performs three basic tasks in completely sequenced bacterial genomes by in silico analysis: PCR amplification, amplified fragment **length** polymorphism (AFLP-PCR) and endonuclease restriction. For PCR, after selection of the genome and introduction of primers, fragment **size**, DNA **sequence** and corresponding open reading frame (ORF) identity of the resulting PCR product is computed. Plasmids of sequenced species may be included in the analysis. Theoretical AFLP-PCR analyzes similar parameters, and includes a suggestion tool providing a list of commercial restriction enzyme pairs yielding up to 50 amplicons in the selected genome. Endonuclease restriction analysis of complete genomes and plasmids calculates the number of restriction **sites** for endonucleases in a given genome. If the number of fragments is 50 or fewer, pulsed field gel electrophoresis image and restriction maps are illustrated. Other tools that have been included in this **site** are ORF search by name and DNA to protein translation as well as restriction digestion of user-defined DNA **sequences**. AVAILABILITY: This is a new molecular biology resource freely available over the Internet at http://www.in-silico.com

L2 ANSWER 4 OF 137 MEDLINE on STN
AN 2004060119 MEDLINE
DN PubMed ID: 14761059
TI Hierarchical analysis of colony and population genetic structure of the eastern subterranean termite, Reticulitermes flavipes, using two classes of molecular markers.
AU Vargo Edward L
CS Department of Entomology, Box 7613, North Carolina State University, Raleigh, North Carolina 27695-7613, USA.. ed_vargo@ncsu.edu
SO Evolution; international journal of organic evolution, (2003 Dec) 57 (12) 2805-18.
Journal code: 0373224. ISSN: 0014-3820.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200402
ED Entered STN: 20040206
Last Updated on STN: 20040221
Entered Medline: 20040220
AB Termites (Isoptera) comprise a large and important group of eusocial insects, yet, in contrast to the eusocial Hymenoptera (ants, bees, wasps), the breeding systems of termites remain poorly understood. In this study, I inferred the breeding system of the subterranean termite Reticulitermes flavipes based on colony and population genetic structure as determined from microsatellite and mitochondrial DNA markers. Termites were sampled from natural wood debris from three undisturbed, forested **sites** in central North Carolina. In each **site**, two transects separated by 1 km were sampled at approximately 15-m intervals. A total of 1272 workers collected from 57 collection points were genotyped at six microsatellite loci, and mitochondrial DNA haplotype was determined for a subset of these individuals using either **restriction**

fragment length polymorphism or **sequence** variation in the AT-rich region. Colonies appeared to be localized: workers from the 57 collection points represented 56 genetically distinct colonies with only a single colony occupying two collection points located 15 m apart. Genetic analysis of family structure and comparisons of estimates of F-statistics (F(IT), F(IC), F(CT)) and coefficients of relatedness (r) among nestmate workers with results of **computer** simulations of potential breeding systems suggested that 77% of all colonies were simple families headed by outbred monogamous pairs, whereas the remaining colonies were extended (inbred) families headed by low numbers of neotenics (about two females and one male) who were the direct offspring of the colony founders. There was no detectable isolation by distance among colonies along transects, suggesting that colony reproduction by budding is not common and that dispersal of reproductives during mating flights is not limited over this distance. Higher-level analysis of the microsatellite loci indicated weak but significant differentiation among **sites** (F(ST) = 0.06), a distance of 16-38 km, and between transects within **sites** (F(ST) = 0.06), a distance of 1 km. No significant differentiation at either the transect or **site** level was detected in the mitochondrial DNA **sequence** data. These results indicate that the study populations of R. flavipes have a breeding system characterized by monogamous pairs of outbred reproductives and relatively low levels of inbreeding because most colonies do not live long enough to produce neotenics, and those colonies that do generate neotenics contain an effectively small number of them.

L2 ANSWER 5 OF 137 MEDLINE on STN
AN 2003354042 MEDLINE
DN PubMed ID: 12842479
TI Detection and identification of Legionella pneumophila by PCR-**restriction fragment length** polymorphism analysis of the RNA polymerase gene (rpoB).
AU Ko Kwan Soo; Hong Seong-Karp; Lee Keun-Hwa; Lee Hae Kyung; Park Mi-Yeoun; Miyamoto Hiroshi; Kook Yoon-Hoh
CS Department of Microbiology and Cancer Research Institute, SNUMRC, Seoul National University College of Medicine, Seoul National University Hospital, 28 Yongon-dong, Chongno-gu, Seoul 110-799, South Korea.
SO Journal of microbiological methods, (2003 Sep) 54 (3) 325-37. Journal code: 8306883. ISSN: 0167-7012.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200311
ED Entered STN: 20030731
Last Updated on STN: 20031218
Entered Medline: 20031117
AB The partial RNA polymerase beta-subunit coding gene (rpoB) **sequences** of 38 Legionella species (59 reference strains) were used to select both Legionella genus-specific and Legionella pneumophila species-specific primers to amplify the 347-bp and 217-bp DNAs, respectively. Enzyme restriction **sites** for PCR-**restriction fragment length** polymorphism (PCR-RFLP) analysis were also generated by a **computer program**. Thirty-eight Legionella species were well differentiated by the identification scheme for Legionella genus-specific PCR-RFLP using HaeIII, AluI, CfoI, PstI, and MaeII. The most common and important pathogenic species, L. pneumophila, was differentiated into two subspecies (L. pneumophila subsp. pneumophila and L. pneumophila subsp. fraseri) by both Legionella genus-specific PCR-RFLP and L. pneumophila species-specific PCR-RFLP using BamHI. Eighty-two Korean culture isolates could also be easily identified by both PCR-RFLP methods as 68 strains of L. pneumophila subsp. pneumophila, 11 strains of L. pneumophila subsp. fraseri, and three novel strains that were separately confirmed by 16S

rDNA and rpoB **sequence** analysis. These results suggest that the rpoB PCR-RFLP for Legionella is a simple and convenient method, not only for specific detection, but also for the rapid identification of Legionella species.

L2 ANSWER 6 OF 137 MEDLINE on STN
AN 2003188854 MEDLINE
DN PubMed ID: 12706667
TI Differentiation of a Vero cell adapted porcine epidemic diarrhea virus from Korean field strains by **restriction fragment length** polymorphism analysis of ORF 3.
AU Song D S; Yang J S; Oh J S; Han J H; Park B K
CS Department of Veterinary Medicine Virology Lab, College of Veterinary Medicine, Seoul National University, Seoul 151-742, Republic of Korea.
SO Vaccine, (2003 May 16) 21 (17-18) 1833-42.
Journal code: 8406899. ISSN: 0264-410X.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200401
ED Entered STN: 20030423
Last Updated on STN: 20040122
Entered Medline: 20040121
AB A porcine epidemic diarrhea virus (PEDV) designated DR13 was isolated in Vero cells and serially passaged by level 100. The virus was titrated at regular intervals of the passage level. Open reading frame (ORF) 3 **sequences** of the virus at passage levels 20, 40, 60, 80, and 100 were aligned and compared using a **computer** software **program**. Suitability of the **restriction fragment length** polymorphism (RFLP) analysis for differentiating the virus from other Korean field strains was investigated. The DR13 field isolate was successively adapted in Vero cells as observed through polymerase chain reaction (PCR) and titration of the virus. RFLP analysis identified change in cleavage **sites** of HindIII and Xho II from passage levels 75 and 90, respectively; these RFLP patterns of ORF 3 differentiated the Vero cell-adapted virus from its parent strain, DR13, and 12 other strains of PEDV studied. The cell adapted DR13 was tested for its pathogenicity and immunogenicity in piglets and pregnant sows. The results indicated that cell adapted DR13 revealed reduced pathogenicity and induced protective immune response in pigs. Differentiation between highly Vero cell-adapted virus and wild-type virus could be the marker of adaptation to cell culture and a valuable tool for epidemiologic studies of PEDV infections. The results of this study supported that the cell attenuated virus could be applied as a marker vaccine candidate against PEDV infection.

L2 ANSWER 7 OF 137 MEDLINE on STN
AN 2003060331 MEDLINE
DN PubMed ID: 12571054
TI Application of new primer-enzyme combinations to terminal **restriction fragment length** polymorphism profiling of bacterial populations in human feces.
AU Nagashima Koji; Hisada Takayoshi; Sato Maremi; Mochizuki Jun
CS Hokkaido Food Processing Research Center, Ebetsu, Hokkaido 069-0836, Japan.. knagashima@foodhokkaido.gr.jp
SO Applied and environmental microbiology, (2003 Feb) 69 (2) 1251-62.
Journal code: 7605801. ISSN: 0099-2240.
CY United States
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AB086439; GENBANK-AB086440; GENBANK-AB086441; GENBANK-AB086442

EM 200304
ED Entered STN: 20030207
Last Updated on STN: 20030417
Entered Medline: 20030415
AB New primer-enzyme combinations for terminal **restriction fragment length** polymorphism (T-RFLP) targeting of the 16S rRNA gene were constructed by using the T-RFLP analysis **program** (designated TAP T-RFLP) located at the Ribosomal Database Project website, and their performance was examined empirically. By using the fluorescently labeled 516f primer (Escherichia coli positions 516 to 532) and 1510r primer (positions 1510 to 1492), the 16S rRNA gene was amplified from human fecal DNA. The resulting amplified product was digested with RsaI plus BfaI or with BslI. When the T-RFLP was carried out with fecal DNAs from eight individuals, eight predominant operational taxonomic units (OTUs) were detected with RsaI and BfaI digestion and 14 predominant OTUs were detected with BslI digestion. The distribution of the OTUs was consistent with the results of the **computer** simulations with TAP T-RFLP. The T-RFLP analyses of the fecal DNAs from individuals gave characteristic profiles, while the variability of the T-RFLP profiles between duplicate DNA preparations from the same samples were minimal. This new T-RFLP method made it easy to predict what kind of intestinal bacterial group corresponded to each OTU on the basis of the terminal **restriction fragment length** compared with the conventional T-RFLP and, moreover, made it possible to identify the bacterial species that an OTU represents by cloning and sequencing.

L2 ANSWER 8 OF 137 MEDLINE on STN
AN 2002727938 MEDLINE
DN PubMed ID: 12490456
TI PCR designer for restriction analysis of various types of **sequence** mutation.
AU Ke Xiayi; Collins Andrew; Ye Shu
CS Wellcome Trust Centre For Human Genetics, University of Oxford, Roosevelt Drive, Oxford OX3 7BN, UK.. xiayi@well.ox.ac.uk
SO Bioinformatics (Oxford, England), (2002 Dec) 18 (12) 1688-9.
Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U03274
EM 200307
ED Entered STN: 20021220
Last Updated on STN: 20030703
Entered Medline: 20030702
AB Restriction analysis is widely used to detect gene mutations such as insertions, deletions and single nucleotide polymorphisms (SNPs). Although such mutation **sites** sometimes present some natural restriction **sites** to differentiate the wild-type and mutant **sequences**, mismatches are often needed in order to create artificial **restriction fragment length** polymorphisms (RFLPs). In this report, a **computer program** is described that screens for suitable restriction enzymes, introducing mismatches where appropriate and when necessary, designs primers using the information of the selected restriction enzymes, their recognition **sequence** and locations as well as the information about the mismatches if any. The **program**, supported by a WWW web interface, is intended to be used online.

L2 ANSWER 9 OF 137 MEDLINE on STN
AN 2002689421 MEDLINE
DN PubMed ID: 12446140
TI Web-based primer design for single nucleotide polymorphism analysis.

AU Neff Michael M; Turk Edward; Kalishman Michael
CS Dept of Biology, Washington University, Campus Box 1137, St Louis, MO 63130-4899, USA.. mneff@biology2.wustl.edu
SO Trends in genetics : TIG, (2002 Dec) 18 (12) 613-5.
Journal code: 8507085. ISSN: 0168-9525.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200301
ED Entered STN: 20021214
Last Updated on STN: 20030122
Entered Medline: 20030121
AB The detection of single nucleotide polymorphisms by PCR is necessary for many types of genetic analysis, from mapping genomes to tracking specific mutations. This technique is most commonly used when polymorphisms alter restriction endonuclease recognition **sites**. Here we describe a web-based **program**, dCAPS Finder 2.0, that facilitates the design of mismatched PCR primers to create or remove a restriction endonuclease recognition **site** relative to the polymorphism being analyzed.

L2 ANSWER 10 OF 137 MEDLINE on STN
AN 2002012976 MEDLINE
DN PubMed ID: 11421118
TI [In silico analysis of the **restriction fragments length** distribution in the human genome].
Analiz in silico raspredelenie restriktnykh fragmentov genoma cheloveka po dlinam.
AU Fedorova L V; Dizadex I; Fedorov A N; Ryskov A P
CS Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, 117984 Russia.
SO Genetika, (2001 Apr) 37 (4) 456-66.
Journal code: 0047354. ISSN: 0016-6758.
CY Russia: Russian Federation
DT Journal; Article; (JOURNAL ARTICLE)
LA Russian
FS Priority Journals
EM 200112
ED Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011221
AB The Restriction On **Computer** (ROC) **program** (freely available at http://www.mcb.harvard.edu/gilbert/ROC) was developed and used to analyze the **restriction fragment length** distribution in the human genome. In contrast to other **programs** searching for restriction **sites**, ROC simultaneously analyzes several long nucleotide **sequences**, such as the entire genomes, and in essence simulates electrophoretic analysis of DNA **restriction fragments**. In addition, this **program** extracts and analyzes DNA repeats that account for peaks in the **restriction fragment length** distribution. The ROC analysis data are consistent with the experimental data obtained via in vitro restriction enzyme analysis (taxonomic printing). A difference between the in vitro and in silico results is explained by underrepresentation of tandem DNA repeats in genomic databases. The ROC analysis of individual genome fragments elucidated the nature of several DNA markers, which were earlier revealed by taxonomic printing, and showed that L1 and Alu repeats are nonrandomly distributed in various chromosomes. Another advantage is that the ROC procedure makes it possible to analyze the nonrandom character of a genomic distribution of short DNA **sequences**. The ROC analysis showed that a low poly(G) frequency is characteristic of the entire human genome, rather than of only coding **sequences**. The method was proposed for a more complex in silico analysis of the genome. For instance, it is

possible to simulate DNA restriction together with blot hybridization and then to analyze the nature of markers revealed.

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=> d his

     (FILE 'HOME' ENTERED AT 10:07:31 ON 03 MAR 2005)

     FILE 'MEDLINE, BIOSIS' ENTERED AT 10:07:39 ON 03 MAR 2005
L1          202 S RESTRICTION FRAGMENT AND SEQUENCE AND SITE AND (COMPUTER OR P
L2          137 S L1 AND (SIZE OR LENGTH)

=> s l2 and (identif? or diagnos?)
L3           65 L2 AND (IDENTIF? OR DIAGNOS?)

=> d 1-10 bib ab

L3   ANSWER 1 OF 65     MEDLINE on STN
AN   2004531454     MEDLINE
DN   PubMed ID: 15500921
TI   Shotgun optical mapping of the entire Leishmania major Friedlin genome.
AU   Zhou Shiguo; Kile Andrew; Kvikstad Erika; Bechner Mike; Severin Jessica;
     Forrest Dan; Runnheim Rod; Churas Chris; Anantharaman Thomas S; Myler
     Peter; Vogt Christy; Ivens Al; Stuart Kenneth; Schwartz David C
CS   Laboratory for Molecular and Computational Genomics, UW Biotechnology
     Center, University of Wisconsin-Madison, 425 Henry Mall, Madison, WI
     53706, USA.
SO   Molecular and biochemical parasitology, (2004 Nov) 138 (1) 97-106.
     Journal code: 8006324. ISSN: 0166-6851.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200502
ED   Entered STN: 20041026
     Last Updated on STN: 20050211
     Entered Medline: 20050210
AB   Leishmania is a group of protozoan parasites which causes a broad spectrum
     of diseases resulting in widespread human suffering and death, as well as
     economic loss from the infection of some domestic animals and wildlife.
     To further understand the fundamental genomic architecture of this
     parasite, and to accelerate the on-going sequencing project, a
     whole-genome XbaI restriction map was constructed using the optical
     mapping system.  This map supplemented traditional physical maps that were
     generated by fingerprinting and hybridization of cosmid and P1 clone
     libraries.  Thirty-six optical map contigs were constructed for the
     corresponding known 36 chromosomes of the Leishmania major Friedlin
     genome.  The chromosome sizes ranged from 326.9 to 2821.3 kb,
     with a total genome size of 34.7 Mb; the average XbaI
     restriction fragment was 25.3 kb, and ranged from 15.7
     to 77.8 kb on a per chromosomes basis.  Comparison between the optical
     maps and the in silico maps of sequence drawn from completed,
     nearly finished, or large sequence contigs showed that optical
     maps served several useful functions within the path to create finished
     sequence by: guiding aspects of the sequence assembly,
     identifying misassemblies, detection of cosmid or PAC clones
     misplacements to chromosomes, and validation of sequence
     stemming from varying degrees of finishing.  Our results also showed the
     potential use of optical maps as a means to detect and characterize map
     segmental duplication within genomes.

L3   ANSWER 2 OF 65     MEDLINE on STN
AN   2004314094     MEDLINE
DN   PubMed ID: 15215682
```

TI The putative recombination of hepatitis B virus genotype B with pre-C/C region of genotype C.
AU Luo Kangxian; Liu Zhihua; He Haitang; Peng Jie; Liang Weifang; Dai Wei; Hou Jinlin
CS Department of Infectious Diseases, Nanfang Hospital, Guangzhou 510515, China.. heplab@fimmu.edu.cn
SO Virus genes, (2004 Aug) 29 (1) 31-41.
Journal code: 8803967. ISSN: 0920-8569.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AY217355; GENBANK-AY217356; GENBANK-AY217357; GENBANK-AY217358; GENBANK-AY217359; GENBANK-AY217360; GENBANK-AY217361; GENBANK-AY217362; GENBANK-AY217363; GENBANK-AY217364; GENBANK-AY217365; GENBANK-AY217366; GENBANK-AY217367; GENBANK-AY217368; GENBANK-AY217369; GENBANK-AY217370; GENBANK-AY217371; GENBANK-AY217372; GENBANK-AY217373; GENBANK-AY217374; GENBANK-AY217375; GENBANK-AY217376; GENBANK-AY217377; GENBANK-AY217378
EM 200410
ED Entered STN: 20040625
Last Updated on STN: 20041022
Entered Medline: 20041021
AB Among hepatitis B virus (HBV) genotypes the B and C are most prevalent in China. To further study on the inside story of the intertypes, the genotype of 136 **sequences** from Chinese patients were analyzed either by **restriction fragment length** polymorphism on fragments or by phylogenetic analysis and bootscanning on full genome. The 22 complete **sequences** of genotype B clustered with different genotypes depending on gene fragments analyzed, which indicated that recombinant events occurred during HBV evolutionary history. To locate the recombinant regions, the **sequences** of HBV entire genome were analyzed by SimPlot **program**. The recombinant regions of B genotype with recombination were mapped in the pre-C/C region with relatively less varied **size**. Besides, three **sequences** of genotype C have recombination with genotype B or D in different regions. However, among all of the 136 **sequences**, none of authentic genotype B was **identified**. To investigate the possible mechanism responsible for intertype recombination, the selection pressure on the recombinant region was estimated by using CODEML **program**. All models allow for positively selected **sites** suggest existence of positive selection pressure. In conclusion, the genotype B with recombination was exclusive subgroup of genotype B in China. The mosaic genotype B might result from immune pressure on the pre-C/C gene.

L3 ANSWER 3 OF 65 MEDLINE on STN
AN 2003354042 MEDLINE
DN PubMed ID: 12842479
TI Detection and **identification** of Legionella pneumophila by PCR-**restriction fragment length** polymorphism analysis of the RNA polymerase gene (rpoB).
AU Ko Kwan Soo; Hong Seong-Karp; Lee Keun-Hwa; Lee Hae Kyung; Park Mi-Yeoun; Miyamoto Hiroshi; Kook Yoon-Hoh
CS Department of Microbiology and Cancer Research Institute, SNUMRC, Seoul National University College of Medicine, Seoul National University Hospital, 28 Yongon-dong, Chongno-gu, Seoul 110-799, South Korea.
SO Journal of microbiological methods, (2003 Sep) 54 (3) 325-37.
Journal code: 8306883. ISSN: 0167-7012.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200311
ED Entered STN: 20030731

Last Updated on STN: 20031218
Entered Medline: 20031117

AB The partial RNA polymerase beta-subunit coding gene (rpoB) **sequences** of 38 Legionella species (59 reference strains) were used to select both Legionella genus-specific and Legionella pneumophila species-specific primers to amplify the 347-bp and 217-bp DNAs, respectively. Enzyme restriction **sites** for PCR-**restriction fragment length** polymorphism (PCR-RFLP) analysis were also generated by a **computer program**. Thirty-eight Legionella species were well differentiated by the **identification** scheme for Legionella genus-specific PCR-RFLP using HaeIII, AluI, CfoI, PstI, and MaeII. The most common and important pathogenic species, L. pneumophila, was differentiated into two subspecies (L. pneumophila subsp. pneumophila and L. pneumophila subsp. fraseri) by both Legionella genus-specific PCR-RFLP and L. pneumophila species-specific PCR-RFLP using BamHI. Eighty-two Korean culture isolates could also be easily **identified** by both PCR-RFLP methods as 68 strains of L. pneumophila subsp. pneumophila, 11 strains of L. pneumophila subsp. fraseri, and three novel strains that were separately confirmed by 16S rDNA and rpoB **sequence** analysis. These results suggest that the rpoB PCR-RFLP for Legionella is a simple and convenient method, not only for specific detection, but also for the rapid **identification** of Legionella species.

L3 ANSWER 4 OF 65 MEDLINE on STN
AN 2003188854 MEDLINE
DN PubMed ID: 12706667
TI Differentiation of a Vero cell adapted porcine epidemic diarrhea virus from Korean field strains by **restriction fragment length** polymorphism analysis of ORF 3.
AU Song D S; Yang J S; Oh J S; Han J H; Park B K
CS Department of Veterinary Medicine Virology Lab, College of Veterinary Medicine, Seoul National University, Seoul 151-742, Republic of Korea.
SO Vaccine, (2003 May 16) 21 (17-18) 1833-42.
Journal code: 8406899. ISSN: 0264-410X.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200401
ED Entered STN: 20030423
Last Updated on STN: 20040122
Entered Medline: 20040121

AB A porcine epidemic diarrhea virus (PEDV) designated DR13 was isolated in Vero cells and serially passaged by level 100. The virus was titrated at regular intervals of the passage level. Open reading frame (ORF) 3 **sequences** of the virus at passage levels 20, 40, 60, 80, and 100 were aligned and compared using a **computer** software **program**. Suitability of the **restriction fragment length** polymorphism (RFLP) analysis for differentiating the virus from other Korean field strains was investigated. The DR13 field isolate was successively adapted in Vero cells as observed through polymerase chain reaction (PCR) and titration of the virus. RFLP analysis **identified** change in cleavage **sites** of HindIII and Xho II from passage levels 75 and 90, respectively; these RFLP patterns of ORF 3 differentiated the Vero cell-adapted virus from its parent strain, DR13, and 12 other strains of PEDV studied. The cell adapted DR13 was tested for its pathogenicity and immunogenicity in piglets and pregnant sows. The results indicated that cell adapted DR13 revealed reduced pathogenicity and induced protective immune response in pigs. Differentiation between highly Vero cell-adapted virus and wild-type virus could be the marker of adaptation to cell culture and a valuable tool for epidemiologic studies of PEDV infections. The results of this study supported that the cell attenuated virus could

be applied as a marker vaccine candidate against PEDV infection.

L3 ANSWER 5 OF 65 MEDLINE on STN
AN 2003060331 MEDLINE
DN PubMed ID: 12571054
TI Application of new primer-enzyme combinations to terminal **restriction fragment length** polymorphism profiling of bacterial populations in human feces.
AU Nagashima Koji; Hisada Takayoshi; Sato Maremi; Mochizuki Jun
CS Hokkaido Food Processing Research Center, Ebetsu, Hokkaido 069-0836, Japan.. knagashima@foodhokkaido.gr.jp
SO Applied and environmental microbiology, (2003 Feb) 69 (2) 1251-62. Journal code: 7605801. ISSN: 0099-2240.
CY United States
DT (EVALUATION STUDIES) Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AB086439; GENBANK-AB086440; GENBANK-AB086441; GENBANK-AB086442
EM 200304
ED Entered STN: 20030207
Last Updated on STN: 20030417
Entered Medline: 20030415
AB New primer-enzyme combinations for terminal **restriction fragment length** polymorphism (T-RFLP) targeting of the 16S rRNA gene were constructed by using the T-RFLP analysis **program** (designated TAP T-RFLP) located at the Ribosomal Database Project website, and their performance was examined empirically. By using the fluorescently labeled 516f primer (Escherichia coli positions 516 to 532) and 1510r primer (positions 1510 to 1492), the 16S rRNA gene was amplified from human fecal DNA. The resulting amplified product was digested with RsaI plus BfaI or with BslI. When the T-RFLP was carried out with fecal DNAs from eight individuals, eight predominant operational taxonomic units (OTUs) were detected with RsaI and BfaI digestion and 14 predominant OTUs were detected with BslI digestion. The distribution of the OTUs was consistent with the results of the **computer** simulations with TAP T-RFLP. The T-RFLP analyses of the fecal DNAs from individuals gave characteristic profiles, while the variability of the T-RFLP profiles between duplicate DNA preparations from the same samples were minimal. This new T-RFLP method made it easy to predict what kind of intestinal bacterial group corresponded to each OTU on the basis of the terminal **restriction fragment length** compared with the conventional T-RFLP and, moreover, made it possible to **identify** the bacterial species that an OTU represents by cloning and sequencing.

L3 ANSWER 6 OF 65 MEDLINE on STN
AN 2001492709 MEDLINE
DN PubMed ID: 11536112
TI Estimating relative population **sizes** from simulated data sets and the question of greater African effective **size**.
AU Eller E
CS Human Genetics Center, University of Texas School of Public Health, Houston, TX 77225, USA.. elise_eller@yahoo.com
SO American journal of physical anthropology, (2001 Sep) 116 (1) 1-12. Journal code: 0400654. ISSN: 0002-9483.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200109
ED Entered STN: 20010906
Last Updated on STN: 20011001
Entered Medline: 20010927

AB Previous genetic and craniometric studies have suggested greater genetic diversity and a larger effective **size** in Africa. Several demographic scenarios can explain a larger African effective **size**, and anthropological geneticists have attempted to obtain better estimates of relative population **sizes** among continental regions in the Old World. A least-squares approach of estimating relative population weights was developed by Relethford and Harpending ([1994] Am. J. Phys. Anthropol. 95:249-270), who applied it to craniometric and genetic data sets and concluded that the ratio of African, Asian, and European effective **sizes** was 3:1:1, respectively; another data set of short tandem repeat (STR) markers yielded a similar estimate of 7:1:2. However, an estimate from restriction **site** polymorphism (RSP, also known as **restriction fragment length** polymorphism, or RFLP) data yielded a very different estimate of 1:1:8. Thus, the European and not the African effective **size** was largest. Simulations showed that this was the result of ascertainment bias in which polymorphic markers were originally **identified** in a small panel of Caucasians, leading to inflated heterozygosity in the European sample and thus an inflated population weight. This paper extends those **computer** simulations to incorporate not only ascertainment bias but also interpopulation gene flow and demographic expansion in two types of genetic data, single nucleotide polymorphisms (SNPs, which are similar but not precisely identical to RSPs) and STRs. The effects of these three parameters on SNP and STR relative weight estimates are described. Simulations show that the ascertainment scheme affects SNP data but not STR data. Gene flow has a noticeable effect on the bias and efficiency of the estimates in both types of genetic data. Population expansions have a large effect only in one ascertainment scheme in the simulated SNP data and no effect in STR data. Relative population weight estimates from four published STR data sets are also reported. These estimates are similar to each other: all show a larger African weight and a European weight somewhat larger than the Asian weight. Because the STR simulations show that when gene flow is greater than 0.01 migrants per generation the African population weight is biased upward, it is likely that the African weights in the four STR data sets are inflated. However, the simulations suggest that the African effective **size** is still largest of the three regions and is probably at least as great as the sum of the Asian and European effective **sizes**.

L3 ANSWER 7 OF 65 MEDLINE on STN
AN 2001407754 MEDLINE
DN PubMed ID: 11459422
TI Effects of ascertainment bias on recovering human demographic history.
AU Eller E
CS Department of Anthropology, University of Utah, Salt Lake City 84112, USA.
SO Human biology; an international record of research, (2001 Jun) 73 (3) 411-27.
Journal code: 0116717. ISSN: 0018-7143.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200108
ED Entered STN: 20010813
Last Updated on STN: 20010813
Entered Medline: 20010809
AB In recent years multilocus data sets have been used to study the demographic history of human populations. In this paper (1) analyses previously done on 60 short tandem repeat (STR) loci are repeated on 30 restriction **site** polymorphism (RSP) markers; (2) relative population weights are estimated from the RSP data set and compared to previously published estimates from STR and craniometric data sets; and

(3) **computer** simulations are performed to show the effects of ascertainment bias on relative population weight estimates. Not surprisingly, given that the RSP markers were originally **identified** in a small panel of Caucasians, estimates of relative population weights are biased and the European population weight is artificially inflated. However, the effects of ascertainment bias are not apparent in a principal components plot or estimates of FST. Ascertainment bias can have a large effect in other genetic systems with inherently low heterozygosity such as Alus or single nucleotide polymorphisms (SNPs), and care must be taken to have prior knowledge of how polymorphic markers in a given data set were originally **identified**. Otherwise, results can be skewed and interpretations faulty.

L3 ANSWER 8 OF 65 MEDLINE on STN
AN 2001317088 MEDLINE
DN PubMed ID: 11393175
TI Genomic growth hormone gene polymorphisms in native Chinese chickens.
AU Ip S C; Zhang X; Leung F C
CS Department of Zoology, The University of Hong Kong, SAR, China.
SO Experimental biology and medicine (Maywood, N.J.), (2001 May) 226 (5) 458-62.
Journal code: 100973463. ISSN: 1535-3702.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200106
ED Entered STN: 20010625
Last Updated on STN: 20010625
Entered Medline: 20010621
AB Chicken growth hormone (cGH), a polypeptide hormone synthesized in and secreted by the pituitary gland, is involved in a wide variety of physiological functions such as growth, body composition, egg production, aging, and reproduction. Chicken growth hormone polymorphisms have been reported to be associated with certain phenotypes. Our objective is to investigate the GH gene polymorphism in selected strains of native Chinese chickens. Yellow Wai Chow GH gene was characterized by sequencing and was found to have one silent substitution, 31 insertions, and other substitutions spread among the introns. In addition, a novel MspI **site** has been **identified** and characterized in the first intron. Allele frequencies of the intron 1 polymorphism were characterized among 28 populations of native Chinese chickens. Thus, polymorphism of the cGH gene may be useful in phylogenetic analysis, as well as in the design of breeding **programs**.

L3 ANSWER 9 OF 65 MEDLINE on STN
AN 2001245495 MEDLINE
DN PubMed ID: 11169256
TI **Identification** of six novel polymorphisms in the human corneodesmosin gene.
AU Guerrin M; Vincent C; Simon M; Tazi Ahnini R; Fort M; Serre G
CS Department of Biology and Pathology of the Cell, INSERM CJF 96-02, Toulouse-Purpan School of Medicine, University of Toulouse III (IFR30, INSERM-CNRS-UPS-CHU), Toulouse, France.
SO Tissue antigens, (2001 Jan) 57 (1) 32-8.
Journal code: 0331072. ISSN: 0001-2815.
CY Denmark
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF224747; GENBANK-AF224748; GENBANK-AF224749; GENBANK-AF224750; GENBANK-AF224751; GENBANK-AF224752; GENBANK-AF224753; GENBANK-AF224754; GENBANK-AF224755; GENBANK-AF224756; GENBANK-AF224757; GENBANK-AF224758;

GENBANK-AF286165
EM 200105
ED Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010510
AB Psoriatic epidermis is characterised by a defective differentiation **program** leading to an abnormal permeability barrier and impaired desquamation. The corneodesmosin gene (CDSN) or "S" gene is a strong candidate in psoriasis susceptibility, due first to its genomic position ("S" gene, 160 kb telomeric to HLA-C) and second to its expression and function in the epidermis. Moreover, an association between CDSN and psoriasis vulgaris was recently shown in Caucasian populations. In order to pursue the CDSN polymorphism analysis, we determined the **sequence** of its alleles in 14 HLA-Cw6-positive individuals. A 4.6 kb genomic fragment encompassing the first exon, the unique intron and the coding **sequence** of the second exon was amplified from 8 psoriatic patients and 6 controls. Allelic discrimination was performed by **restriction fragment length** polymorphism analysis. The entire coding **sequence** and the intron boundaries of 27 alleles were sequenced. A total of 26 dimorphic **sites** were found, 23 consisting in single nucleotide polymorphisms (SNPs) and 3 in triplet modifications. Five out of the 23 SNPs have not been previously reported, and among them, one causes amino-acid exchange leading to the suppression of a potential chymotrypsin **site**. Among the triplet modifications, one leads to deletion of one out of five consecutive valines in the protein. The high polymorphism of the gene allowed the **identification** of 13 different alleles. These haplotypes will permit additional family-based studies that could provide new genetic support for the involvement of CDSN in psoriasis susceptibility. Moreover, the establishment of an extensive catalogue of CDSN alleles will allow functional analyses of the different protein isoforms.

L3 ANSWER 10 OF 65 MEDLINE on STN
AN 2001186385 MEDLINE
DN PubMed ID: 11266565
TI GenEST, a powerful bidirectional link between cDNA **sequence** data and gene expression profiles generated by cDNA-AFLP.
AU Qin L; Prins P; Jones J T; Popeijus H; Smant G; Bakker J; Helder J
CS The Graduate School for Experimental Plant Sciences, Laboratory of Nematology, Wageningen University and Research Center, Binnenhaven 10, 6709 PD Wageningen, The Netherlands.. ling.qin@nema.dpw.wau.nl
SO Nucleic acids research, (2001 Apr 1) 29 (7) 1616-22.
Journal code: 0411011. ISSN: 1362-4962.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200105
ED Entered STN: 20010517
Last Updated on STN: 20010521
Entered Medline: 20010503
AB The release of vast quantities of DNA **sequence** data by large-scale genome and expressed **sequence** tag (EST) projects underlines the necessity for the development of efficient and inexpensive ways to link **sequence** databases with temporal and spatial expression profiles. Here we demonstrate the power of linking cDNA **sequence** data (including EST **sequences**) with transcript profiles revealed by cDNA-AFLP, a highly reproducible differential display method based on restriction enzyme digests and selective amplification under high stringency conditions. We have developed a **computer program** (GenEST) that predicts the **sizes** of virtual transcript-derived fragments (TDFs) of in silico-digested cDNA **sequences** retrieved from databases. The vast majority of the

resulting virtual TDFs could be traced back among the thousands of TDFs displayed on cDNA-AFLP gels. Sequencing of the corresponding bands excised from cDNA-AFLP gels revealed no inconsistencies. As a consequence, cDNA **sequence** databases can be screened very efficiently to **identify** genes with relevant expression profiles. The other way round, it is possible to switch from cDNA-AFLP gels to **sequences** in the databases. Using the restriction enzyme recognition **sites**, the primer extensions and the estimated TDF **size** as **identifiers**, the DNA **sequence**(s) corresponding to a TDF with an interesting expression pattern can be **identified**. In this paper we show examples in both directions by analyzing the plant parasitic nematode Globodera rostochiensis. Various novel pathogenicity factors were **identified** by combining ESTs from the infective stage juveniles with expression profiles of approximately 4000 genes in five developmental stages produced by cDNA-AFLP.

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L3 ANSWER 11 OF 65 MEDLINE on STN
AN 2001144875 MEDLINE
DN PubMed ID: 11132490
TI Human DNA polymorphism of HaeIII system in Chinese oriental, Han population.
AU Li S B; Hu H T; Rèn H M; Li Z D
CS Forensic Science College, Xian Medical University, Xi'an 710061, China.
SO Yi chuan xue bao = Acta genetica Sinica, (2000) 27 (9) 753-61.
Journal code: 7900784. ISSN: 0379-4172.
CY China
DT Journal; Article; (JOURNAL ARTICLE)
LA Chinese
FS Priority Journals
EM 200103
ED Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010315
AB DNA typing by **restriction fragment length** polymorphism (RFLP) analysis was an extremely important technique used in forensic science **identification**, paternity test and gene **diagnosis**. While RFLP testing was a highly informative method, it traditionally had several disadvantages. It was time consuming and involved in working with radioactive phosphorus. A chemiluminescent detection of RFLP technique that was faster and safer than isotopic detection. The chemiluminescent system had a good sensitivity of detecting 3-25 ng sample DNA. The development of direct alkaline phosphatase (AP) conjugated probes and improved chemiluminescent substrates provided a non-isotopic detection method that equaled or surpassed 32P detection systems. Population genetic studies were performed using direct alkaline phosphatase (AP) conjugated oligonucleotide probes (AL1874, YNH24, TBQ7, VI) that recognized four hypervariable number of tandem repeats regions (D2S92, D2S44, D10S28, D17S79 loci) respectively in the human genome. DNA from approximately 480 unrelated individuals, subdivided into oriental group were digested with HaeIII enzyme and were successively hybridized to each DNA probe. The number of distinct DNA fragments **identified** for each of these regions varies from 37 to more than 78. An allele frequency distribution was determined for each locus with the **computer** and digitizer. The results showed significant differences between different races (American-blacks, Caucasians, and Orientals), in the pattern of distributions as well as in the relative frequency of the most common alleles of D2S92, D2S44, D10S28, and D17S79. The results showed that the analysis of these loci had useful applications in genetics and in forensic identity.

L3 ANSWER 12 OF 65 MEDLINE on STN
AN 2001018406 MEDLINE
DN PubMed ID: 10907085
TI Fingerprinting method for phylogenetic classification and **identification** of microorganisms based on variation in 16S rRNA gene **sequences**.
AU Raghava G P; Solanki R J; Soni V; Agrawal P
CS Institute of Microbial Technology, Chandigarh, India.
SO BioTechniques, (2000 Jul) 29 (1) 108-12, 114-6.
Journal code: 8306785. ISSN: 0736-6205.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200011
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001109
AB The paper describes a method for the classification and **identification** of microorganisms based on variations in 16S rRNA **sequences**. The 16S rRNA is one of the most conserved molecules within a cell. The nature of the variable and spacer regions has been found to be specific to a given organism. Thus, the method presented here can be very useful for the classification and **identification** of microorganisms for which very little information is available. To automate the method, a comprehensive **computer program** called FPMAP has been developed for the analysis of **restriction fragment** pattern data. The method involves the restriction digestion of genomic DNA, preferably using four-cutters that may recognize 6-9 **sites** within the 16S rDNA. The fragments are separated on a polyacrylamide gel along with a suitable marker, then transferred into a nylon membrane and hybridized with a radiolabeled 16S rDNA probe. After autoradiography, the fragment **sizes** are calculated, and the data are analyzed using the FPMAP software. We demonstrate that the method can be used for **identification** of strains of Streptomyces and mycobacteria. The software is available from our ftp **site** ftp: imtech.chd.nic.in/pub/com/fpmap/unix/.

L3 ANSWER 13 OF 65 MEDLINE on STN
AN 2000266556 MEDLINE
DN PubMed ID: 10806593
TI Primer system for single cell detection of double mutation for Tay-Sachs disease.
AU Liu M C; Drury K C; Kipersztok S; Zheng W; Williams R S
CS Department of Obstetrics and Gynecology, College of Medicine, University of Florida, Gainesville 32610, USA.
SO Journal of assisted reproduction and genetics, (2000 Feb) 17 (2) 121-6.
Journal code: 9206495. ISSN: 1058-0468.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200007
ED Entered STN: 20000720
Last Updated on STN: 20000720
Entered Medline: 20000710
AB PURPOSE: Nearly 100% of infantile Tay-Sachs disease is produced by two mutations occurring in the alpha chain of the lysosomal enzyme beta-N-acetylhexosaminidase (HEXA) in the Ashkenazi Jewish population. Although others have described primer systems used to amplify both **sites** simultaneously, few discuss the allele dropout problems inherent in this test. Our goal was to construct a more robust test enabling stronger signal generation for single cell preimplantation

genetic **diagnosis** and to investigate the occurrence of allele dropout. METHODS: New nested primers were designed to optimize detection of both major Tay-Sachs mutations. Four hundred fifty-seven single cells, including normal cells and those carrying mutations of either the 4bp insertion exon 11 or splice-**site** intron 12 defects, were used to screen a new primer system. RESULTS: Based on PCR amplified product analysis, total efficiency of amplification was 85.3%, (390/457). The allele dropout rate for the 4bp insertion mutation in exon 11 and splice-**site** mutation in intron 12 was 4.8% and 5.8%, respectively. CONCLUSIONS: Multiple mutation detection and analysis within the Tay-Sachs disease gene (HEXA) is possible using single cells for clinical preimplantation genetic **diagnosis**. Alternative PCR primers and conditions offer various methods for developing systems compatible to specific **program** requirements.

L3 ANSWER 14 OF 65 MEDLINE on STN
AN 2000250973 MEDLINE
DN PubMed ID: 10790088
TI **Identification** of a novel DNA probe for strain typing Mycobacterium bovis by **restriction fragment length** polymorphism analysis.
AU O'Brien R; Flynn O; Costello E; O'Grady D; Rogers M
CS National Agricultural and Veterinary Biotechnology Centre, University College Dublin, Belfield, Dublin 4, Ireland.. rory.obrien@ucd.ie
SO Journal of clinical microbiology, (2000 May) 38 (5) 1723-30. Journal code: 7505564. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200006
ED Entered STN: 20000629
Last Updated on STN: 20000629
Entered Medline: 20000621
AB Bovine tuberculosis caused by Mycobacterium bovis remains a significant disease of farmed cattle in many countries despite ongoing tuberculosis eradication **programs**. Molecular typing methods such as **restriction fragment length** polymorphism (RFLP) analysis and spoligotyping have been used to **identify** related herd breakdowns in an attempt to **identify** more precisely the route of infection into cattle herds and to trace the transmission of bovine tuberculosis. A recent geographical survey of Irish M. bovis isolates demonstrated that a significant proportion of isolates (approximately 20%) exhibit a common strain type, limiting the value of current strain typing methods as an epidemiological tool. We have **identified** and cloned a region of the M. bovis genome, pUCD, which generates a clear, highly polymorphic banding pattern when used as an RFLP probe on AluI restriction-digested M. bovis genomic DNA and which effectively subdivides this common strain type. When used to type 60 Irish M. bovis isolates, pUCD exhibited greater discriminatory power than the commonly used mycobacterial RFLP probes IS6110, PGRS, and DR and detected an equivalent number of strain types to a combination of these three probes. pUCD also detected significantly more strain types than the spoligotyping technique, while maintaining a high level of concordance between epidemiologically related and unrelated herd breakdowns. The polymorphic element within pUCD remains to be fully characterized, however the potential for this probe to greatly decrease the workload necessary to genotype M. bovis by RFLP analysis is compelling.

L3 ANSWER 15 OF 65 MEDLINE on STN
AN 2000156344 MEDLINE
DN PubMed ID: 10689173
TI Response of soybean rhizosphere communities to human hygiene water addition as determined by community level physiological profiling (CLPP)

and terminal **restriction fragment length** polymorphism (TRFLP) analysis.
AU Kerkhof L; Santoro M; Garland J
CS Institute of Marine and Coastal Sciences, Rutgers University, New Brunswick, NJ 08901-8521, USA.. kerkof@imcs.rutgers.edu
SO FEMS microbiology letters, (2000 Mar 1) 184 (1) 95-101.
Journal code: 7705721. ISSN: 0378-1097.
(Investigators: Garland J, KSC)
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Space Life Sciences
EM 200004
ED Entered STN: 20000505
Last Updated on STN: 20000505
Entered Medline: 20000421
AB In this report, we describe an experiment conducted at Kennedy Space Center in the biomass production chamber (BPC) using soybean plants for purification and processing of human hygiene water. Specifically, we tested whether it was possible to detect changes in the root-associated bacterial assemblage of the plants and ultimately to **identify** the specific microorganism(s) which differed when plants were exposed to hygiene water and other hydroponic media. Plants were grown in hydroponics media corresponding to four different treatments: control (Hoagland's solution), artificial gray water (Hoagland's+surfactant), filtered gray water collected from human subjects on **site**, and unfiltered gray water. Differences in rhizosphere microbial populations in all experimental treatments were observed when compared to the control treatment using both community level physiological profiles (BIOLOG) and molecular fingerprinting of 16S rRNA genes by terminal **restriction fragment length** polymorphism analysis (TRFLP). Furthermore, screening of a clonal library of 16S rRNA genes by TRFLP yielded nearly full **length** SSU genes associated with the various treatments. Most 16S rRNA genes were affiliated with the Klebsiella, Pseudomonas, Variovorax, Burkholderia, Bordetella and Isosphaera groups. This molecular approach demonstrated the ability to rapidly detect and **identify** microorganisms unique to experimental treatments and provides a means to fingerprint microbial communities in the biosystems being developed at NASA for optimizing advanced life support operations.

L3 ANSWER 16 OF 65 MEDLINE on STN
AN 2000129296 MEDLINE
DN PubMed ID: 10667834
TI Analysis of point mutation in exon 2 of CYP2E1 gene in renal cell/urothelial cancer patients in comparison with control population.
AU Farker K; Lehmann M H; Kastner R; Weber J; Janitzky V; Schubert J; Hoffmann A
CS Institute of Clinical Pharmacology, Jena, Germany.
SO International journal of clinical pharmacology and therapeutics, (2000 Jan) 38 (1) 30-4.
Journal code: 9423309. ISSN: 0946-1965.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200003
ED Entered STN: 20000320
Last Updated on STN: 20000320
Entered Medline: 20000308
AB OBJECTIVE: Genetic polymorphisms of human cytochrome P450s have been implicated to be of importance for susceptibility to different cancers. Recently, a point mutation was found in the exon 2 of the CYP2E1 gene (CYP2E1*2) [Hu et al. 1997]. In order to evaluate a possible link between the point mutation in exon 2 of the CYP2E1 gene and the susceptibility to

renal cell/urothelial cancer, we developed a screening method based on the polymerase chain reaction (PCR) and **restriction fragment length** polymorphism (RFLP). MATERIAL: DNA of peripheral white blood cells was isolated from 158 renal cell/urothelial cancer patients as well as from 150 controls. METHOD: Primers for PCR were designed by the Primer 3 release 0.1 **program**. The PCR yield a product of 215 base pairs (bp), which was digested with the restriction enzyme Hha I. The DNA fragments were separated on a 3% agarose gel stained with ethidium bromide. Restriction enzyme digestion of the PCR product obtained from the wild-type DNA resulted in the appearance of a 66 bp, a 43 bp, a 40 bp, a 39 bp and a 28 bp DNA fragment. In contrast to the wild-type, the digestion of the PCR product from DNA carrying the point mutation resulted in the loss of the 39 bp and 40 bp fragments and the appearance of an additional 79 bp fragment. Therefore, the loss of one Hha I restriction **site** caused by a single nucleotide exchange is suitable for the **identification** of the point mutation in exon 2 of CYP2E1 gene. RESULTS: However, we could not detect any point mutation in any of the 158 renal cell/urothelial cancer patients or the 150 controls. The distribution of the point mutation in exon 2 of CYP2E1 gene did not show any difference in renal cell/urothelial cancer patients and controls. CONCLUSION: This might indicate a lack of association between this CYP2E polymorphism (CYP2E1*2) and renal cell/urothelial cancer.

L3 ANSWER 17 OF 65 MEDLINE on STN
AN 1999450166 MEDLINE
DN PubMed ID: 10520448
TI Bovine ornithine decarboxylase gene: cloning, structure and polymorphisms.
AU Yao J; Zadworny D; Aggrey S E; Kuhnlein U; Hayes J F
CS Dept. of Animal Science, McGill University, Quebec, Canada.
SO DNA sequence : journal of DNA sequencing and mapping, (1998 Mar) 8 (4) 203-13.
Journal code: 9107800. ISSN: 1042-5179.
CY Switzerland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U36394
EM 199912
ED Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991202
AB Bovine ornithine decarboxylase (ODC) genomic clones were isolated from a bacteriophage lambda DASH genomic library. A total of 9452 bp **sequence** was determined which covers the entire **sequence** of the bovine ODC gene. **Sequence** analysis showed that the bovine ODC gene consisted of 12 exons which encode a protein identical to that inferred from a bovine ODC cDNA. Comparison of the structure and nucleotide **sequence** of the bovine, human and mouse ODC genes revealed that the gene was highly conserved. Primer extension analysis demonstrated that the transcription start point of bovine ODC mRNA was located 378 bp upstream from the A residue in the translation initiation codon. The 5'-untranslated region (UTR) of ODC mRNA was highly G + C rich, particularly in its 5'-most portion, and **computer** predictions suggested a very stable secondary structure for this region, with an overall free energy of formation of -134.4 kcal/mol. Conserved **sequences** and potential promoter elements including a TATA box, a possible CCAAT element, SP1 ranscription factor binding **sites** (GC boxes) and cAMP response elements (CRE) were **identified** in the 5'-flanking region of the gene. Two polymorphic restriction **sites**, a TaqI and a MspI, were mapped to the ODC gene and PCR-based methods for detection of the 2 polymorphisms were developed.

L3 ANSWER 18 OF 65 MEDLINE on STN
AN 1999441476 MEDLINE

DN PubMed ID: 10511805
TI The application of end user computing (EUC) for detection of lipoprotein lipase gene abnormality.
AU Li J; Kobori K; Kondo A; Yonekawa O; Kanno T
CS Department of Laboratory Medicine, Hamamatsu University School of Medicine.
SO Rinsho byori. Japanese journal of clinical pathology, (1999 Aug) 47 (8) 737-43.
Journal code: 2984781R. ISSN: 0047-1860.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA Japanese
FS Priority Journals
EM 199910
ED Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991029
AB Lipoprotein lipase (LPL) is an enzyme digesting lipoprotein triglyceride (TG) in peripheral blood vessels. Most patients with LPL deficiency show very high plasma TG and low HDL-C. To establish an effective **computer**-based screening system to **identify** individuals with genetic LPL disorders, we selected 50 subjects whose plasma TG was over 350mg/dl and HDL-C was lower than 35mg/dl from patients at Hamamatsu University Hospital. We applied End User Computing (EUC) of our laboratory system to select high risk subjects with LPL gene abnormalities. Polymerase chain reaction (PCR) products from LPL gene exons 2-9 were screened by single-strand conformation polymorphism (SSCP), direct DNA **sequence** analysis and **restriction fragment length** polymorphism (RFLP). We found a novel missense mutation (1223C-->G, S323C) in LPL gene exon 7 from three subjects. By PCR-mediated **site**-directed mutagenesis and restriction digestion, the three subjects were found to be heterozygous. In addition, we **identified** two other common mutations in Japanese employing the RFLP method. One was the 1595C-->G (S447X) in exon 9 from six subjects, two homozygous and four heterozygous individuals. The other was a mutation of intron 3 (C-->T transition) from four heterozygous subjects. Using EUC screening method, we detected genetic LPL abnormalities more easily. The frequency of the LPL gene mutation in the 50 high-risk subjects was 26%, and was estimated to be one out of 2,000 patients at our clinic. Using the EUC system to screen for LPL mutations was established to be an effective **computer**-based screening system to **identify** individuals with genetic abnormalities.

L3 ANSWER 19 OF 65 MEDLINE on STN
AN 1999408143 MEDLINE
DN PubMed ID: 10480266
TI Use of PCR-**restriction fragment length** polymorphism analysis of the hsp65 gene for rapid **identification** of mycobacteria in Brazil.
AU da Silva Rocha A; da Costa Leite C; Torres H M; de Miranda A B; Pires Lopes M Q; Degrave W M; Suffys P N
CS Department of Biochemistry and Molecular Biology, Oswaldo Cruz Institute, Oswaldo Cruz Foundation, Rio de Janeiro, Brazil.
SO Journal of microbiological methods, (1999 Sep) 37 (3) 223-9.
Journal code: 8306883. ISSN: 0167-7012.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-M15467; GENBANK-U55826; GENBANK-U55829; GENBANK-U55834
EM 199910
ED Entered STN: 19991101
Last Updated on STN: 19991101

Entered Medline: 19991021

AB Polymerase chain reaction amplification of part of the gene coding for the heat shock protein hsp65 followed by restriction enzyme analysis (PRA) is a recently described tool for rapid **identification** of mycobacteria. In this study, the speed and simplicity of PRA for **identification** of isolates of mycobacteria from patients with clinical symptoms of tuberculosis was evaluated and compared with **identification** results obtained by commercially available methods. Established PRA patterns were observed for nineteen isolates of Mycobacterium tuberculosis, eleven belonging to the complex M. avium-intracellulare, four of M. kansasii, one of M. fortuitum, one of M. abscessus, three of M. gordonae and one of the recently described species M. lentiflavum, as **identified** by commercially available methods. Two isolates of M. fortuitum and one of M. gordonae had unique and so far undescribed PRA patterns, suggesting geographically-related intra-species variation within the hsp65 **sequence**. We propose the inclusion of these new patterns in the PRA **identification** algorithm and have defined more accurately the molecular weight values of the **restriction fragments**. This is the first report on the isolation of M. lentiflavum in Brazil suggesting that **identification** by means of PRA could be useful for detection of mycobacterial species that are usually unnoticed. Where the use of several commercial techniques in combination was necessary for correct **identification**, PRA demonstrated to be a simple technique with good cost-benefit for characterization of all mycobacterial isolates in this study.

L3 ANSWER 20 OF 65 MEDLINE on STN
AN 1999331615 MEDLINE
DN PubMed ID: 10404729
TI Three point mutations of human butyrylcholinesterase in a Japanese family and the alterations of three-dimensional structure.
AU Asanuma K; Yagihashi A; Uehara N; Kida T; Watanabe N
CS Department of Laboratory Diagnosis, Sapporo Medical University School of Medicine, Japan.
SO Clinica chimica acta; international journal of clinical chemistry, (1999 May) 283 (1-2) 33-42.
Journal code: 1302422. ISSN: 0009-8981.
CY Netherlands
DT (CASE REPORTS)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199908
ED Entered STN: 19990910
Last Updated on STN: 19990910
Entered Medline: 19990824

AB Three different mutations at codons 330 (TTA to ATA), 365 (GGA to AGA) and 515 (CGT to TGT) of human butyrylcholinesterase (hBChE) were **identified** in a Japanese family. We correlated alterations in in the patient's hBChE activity with possible structural alterations in the three-dimensional structure of hBChE caused by the point mutations. This study was performed using the published **computer**-generated three-dimensional structure of hBChE based on the structure of acetylcholinesterase. The amino acid substitution at L330I was adjacent to hydrophobic residues that form the channel domain of the active center. This side chain faced the side opposite the active center. The amino acid substitution at G365R was located at the position most remote from the active center, and this substitution **site** was exposed to the surface of the BChE protein. Alpha-helical structure was present to the active center, and the guanidyl residue of native Arg 515 was hydrogen-bonded to the carboxyl group of Asp 395 in the alpha-helix. These point mutations may cause steric effects on the present patient's hBChE activity. This is the first report of three-dimensional structural

analysis performed on the L330I, G365R, and R515C mutations of hBChE.

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FILE 'MEDLINE, BIOSIS' ENTERED AT 10:07:39 ON 03 MAR 2005
L1 202 S RESTRICTION FRAGMENT AND SEQUENCE AND SITE AND (COMPUTER OR P
L2 137 S L1 AND (SIZE OR LENGTH)
L3 65 S L2 AND (IDENTIF? OR DIAGNOS?)

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L4 83 L2 AND PY<2001

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L4 ANSWER 1 OF 83 MEDLINE on STN
AN 2001144875 MEDLINE
DN PubMed ID: 11132490
TI Human DNA polymorphism of HaeIII system in Chinese oriental, Han population.
AU Li S B; Hu H T; Ren H M; Li Z D
CS Forensic Science College, Xian Medical University, Xi'an 710061, China.
SO Yi chuan xue bao = Acta genetica Sinica, **(2000)** 27 (9) 753-61.
Journal code: 7900784. ISSN: 0379-4172.
CY China
DT Journal; Article; (JOURNAL ARTICLE)
LA Chinese
FS Priority Journals
EM 200103
ED Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010315
AB DNA typing by **restriction fragment length** polymorphism (RFLP) analysis was an extremely important technique used in forensic science identification, paternity test and gene diagnosis. While RFLP testing was a highly informative method, it traditionally had several disadvantages. It was time consuming and involved in working with radioactive phosphorus. A chemiluminescent detection of RFLP technique that was faster and safer than isotopic detection. The chemiluminescent system had a good sensitivity of detecting 3-25 ng sample DNA. The development of direct alkaline phosphatase (AP) conjugated probes and improved chemiluminescent substrates provided a non-isotopic detection method that equaled or surpassed 32P detection systems. Population genetic studies were performed using direct alkaline phosphatase (AP) conjugated oligonucleotide probes (AL1874, YNH24, TBQ7, VI) that recognized four hypervariable number of tandem repeats regions (D2S92, D2S44, D10S28, D17S79 loci) respectively in the human genome. DNA from approximately 480 unrelated individuals, subdivided into oriental group were digested with HaeIII enzyme and were successively hybridized to each DNA probe. The number of distinct DNA fragments identified for each of these regions varies from 37 to more than 78. An allele frequency distribution was determined for each locus with the **computer** and digitizer. The results showed significant differences between different races (American-blacks, Caucasians, and Orientals), in the pattern of distributions as well as in the relative frequency of the most common alleles of D2S92, D2S44, D10S28, and D17S79. The results showed that the analysis of these loci had useful applications in genetics and in forensic identity.

L4 ANSWER 2 OF 83 MEDLINE on STN
AN 2001075810 MEDLINE

DN PubMed ID: 10919828
TI Terminal **restriction fragment length** polymorphism analysis **program**, a web-based research tool for microbial community analysis.
AU Marsh T L; Saxman P; Cole J; Tiedje J
CS Center for Microbial Ecology, Michigan State University, East Lansing, Michigan 48824, USA.. MARSHT@pilot.msu.edu
SO Applied and environmental microbiology, **(2000 Aug)** 66 (8) 3616-20.
Journal code: 7605801. ISSN: 0099-2240.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200101
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010104
AB Rapid analysis of microbial communities has proven to be a difficult task. This is due, in part, to both the tremendous diversity of the microbial world and the high complexity of many microbial communities. Several techniques for community analysis have emerged over the past decade, and most take advantage of the molecular phylogeny derived from 16S rRNA comparative **sequence** analysis. We describe a web-based research tool located at the Ribosomal Database Project web **site** (http://www.cme.msu.edu/RDP/html/analyses. html) that facilitates microbial community analysis using terminal **restriction fragment length** polymorphism of 16S ribosomal DNA. The analysis function (designated TAP T-RFLP) permits the user to perform in silico restriction digestions of the entire 16S **sequence** database and derive terminal **restriction fragment sizes**, measured in base pairs, from the 5' terminus of the user-specified primer to the 3' terminus of the restriction endonuclease target **site**. The output can be sorted and viewed either phylogenetically or by **size**. It is anticipated that the **site** will guide experimental design as well as provide insight into interpreting results of community analysis with terminal **restriction fragment length** polymorphisms.

L4 ANSWER 3 OF 83 MEDLINE on STN
AN 2001018406 MEDLINE
DN PubMed ID: 10907085
TI Fingerprinting method for phylogenetic classification and identification of microorganisms based on variation in 16S rRNA gene **sequences**.
AU Raghava G P; Solanki R J; Soni V; Agrawal P
CS Institute of Microbial Technology, Chandigarh, India.
SO BioTechniques, **(2000 Jul)** 29 (1) 108-12, 114-6.
Journal code: 8306785. ISSN: 0736-6205.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200011
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001109
AB The paper describes a method for the classification and identification of microorganisms based on variations in 16S rRNA **sequences**. The 16S rRNA is one of the most conserved molecules within a cell. The nature of the variable and spacer regions has been found to be specific to a given organism. Thus, the method presented here can be very useful for the classification and identification of microorganisms for which very little information is available. To automate the method, a comprehensive **computer program** called FPMAP has been developed for the

analysis of **restriction fragment** pattern data. The method involves the restriction digestion of genomic DNA, preferably using four-cutters that may recognize 6-9 **sites** within the 16S rDNA. The fragments are separated on a polyacrylamide gel along with a suitable marker, then transferred into a nylon membrane and hybridized with a radiolabeled 16S rDNA probe. After autoradiography, the fragment **sizes** are calculated, and the data are analyzed using the FPMAP software. We demonstrate that the method can be used for identification of strains of Streptomyces and mycobacteria. The software is available from our ftp **site** ftp: imtech.chd.nic.in/pub/com/fpmap/unix/.

L4 ANSWER 4 OF 83 MEDLINE on STN
AN 2000266556 MEDLINE
DN PubMed ID: 10806593
TI Primer system for single cell detection of double mutation for Tay-Sachs disease.
AU Liu M C; Drury K C; Kipersztok S; Zheng W; Williams R S
CS Department of Obstetrics and Gynecology, College of Medicine, University of Florida, Gainesville 32610, USA.
SO Journal of assisted reproduction and genetics, **(2000 Feb)** 17 (2) 121-6.
Journal code: 9206495. ISSN: 1058-0468.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200007
ED Entered STN: 20000720
Last Updated on STN: 20000720
Entered Medline: 20000710
AB PURPOSE: Nearly 100% of infantile Tay-Sachs disease is produced by two mutations occurring in the alpha chain of the lysosomal enzyme beta-N-acetylhexosaminidase (HEXA) in the Ashkenazi Jewish population. Although others have described primer systems used to amplify both **sites** simultaneously, few discuss the allele dropout problems inherent in this test. Our goal was to construct a more robust test enabling stronger signal generation for single cell preimplantation genetic diagnosis and to investigate the occurrence of allele dropout. METHODS: New nested primers were designed to optimize detection of both major Tay-Sachs mutations. Four hundred fifty-seven single cells, including normal cells and those carrying mutations of either the 4bp insertion exon 11 or splice-**site** intron 12 defects, were used to screen a new primer system. RESULTS: Based on PCR amplified product analysis, total efficiency of amplification was 85.3%, (390/457). The allele dropout rate for the 4bp insertion mutation in exon 11 and splice-**site** mutation in intron 12 was 4.8% and 5.8%, respectively. CONCLUSIONS: Multiple mutation detection and analysis within the Tay-Sachs disease gene (HEXA) is possible using single cells for clinical preimplantation genetic diagnosis. Alternative PCR primers and conditions offer various methods for developing systems compatible to specific **program** requirements.

L4 ANSWER 5 OF 83 MEDLINE on STN
AN 2000250973 MEDLINE
DN PubMed ID: 10790088
TI Identification of a novel DNA probe for strain typing Mycobacterium bovis by **restriction fragment length** polymorphism analysis.
AU O'Brien R; Flynn O; Costello E; O'Grady D; Rogers M
CS National Agricultural and Veterinary Biotechnology Centre, University College Dublin, Belfield, Dublin 4, Ireland.. rory.obrien@ucd.ie
SO Journal of clinical microbiology, **(2000 May)** 38 (5) 1723-30.
Journal code: 7505564. ISSN: 0095-1137.
CY United States

DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200006
ED Entered STN: 20000629
Last Updated on STN: 20000629
Entered Medline: 20000621
AB Bovine tuberculosis caused by Mycobacterium bovis remains a significant disease of farmed cattle in many countries despite ongoing tuberculosis eradication **programs**. Molecular typing methods such as **restriction fragment length** polymorphism (RFLP) analysis and spoligotyping have been used to identify related herd breakdowns in an attempt to identify more precisely the route of infection into cattle herds and to trace the transmission of bovine tuberculosis. A recent geographical survey of Irish M. bovis isolates demonstrated that a significant proportion of isolates (approximately 20%) exhibit a common strain type, limiting the value of current strain typing methods as an epidemiological tool. We have identified and cloned a region of the M. bovis genome, pUCD, which generates a clear, highly polymorphic banding pattern when used as an RFLP probe on AluI restriction-digested M. bovis genomic DNA and which effectively subdivides this common strain type. When used to type 60 Irish M. bovis isolates, pUCD exhibited greater discriminatory power than the commonly used mycobacterial RFLP probes IS6110, PGRS, and DR and detected an equivalent number of strain types to a combination of these three probes. pUCD also detected significantly more strain types than the spoligotyping technique, while maintaining a high level of concordance between epidemiologically related and unrelated herd breakdowns. The polymorphic element within pUCD remains to be fully characterized, however the potential for this probe to greatly decrease the workload necessary to genotype M. bovis by RFLP analysis is compelling.

L4 ANSWER 6 OF 83 MEDLINE on STN
AN 2000190472 MEDLINE
DN PubMed ID: 10726273
TI RFLP analysis of PCR-amplified small subunit ribosomal DNA of three fish microsporidian species.
AU Leiro J; Siso M I; Parama A; Ubeira F M; Sanmartin M L
CS Laboratorio de Parasitologia, Facultad de Farmacia, Universidad de Santiago de Compostela, Spain.. mpleiro@usc.es
SO Parasitology, **(2000 Feb)** 120 (Pt 2) 113-9.
Journal code: 0401121. ISSN: 0031-1820.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200004
ED Entered STN: 20000427
Last Updated on STN: 20000427
Entered Medline: 20000420
AB The phylogenetic relationships of the microsporidian species Microgemma caulleryi, Pleistophora finisterrensis and Tetramicra brevifilum were investigated on the basis of **restriction fragment length** polymorphism (RFLP) analysis of PCR-amplified small-subunit rDNA (SSUrDNA). Using PCR primers specific for microsporidian SSUrDNA, a single product was obtained from each species, and heteroduplex analysis indicated a high degree of **sequence** homology among the 3 products. In RFLP analysis of the PCR-amplified SSUrDNA, the enzymes AluI and DdeI gave restriction patterns that differed among all 3 species. Phylogenetic analysis using restriction patterns as differential characters indicated that Microgemma caulleryi and Tetramicra brevifilum are more closely related to each other than to Pleistophora finisterrensis.

L4 ANSWER 7 OF 83 MEDLINE on STN
AN 2000156344 MEDLINE
DN PubMed ID: 10689173
TI Response of soybean rhizosphere communities to human hygiene water addition as determined by community level physiological profiling (CLPP) and terminal **restriction fragment length** polymorphism (TRFLP) analysis.
AU Kerkhof L; Santoro M; Garland J
CS Institute of Marine and Coastal Sciences, Rutgers University, New Brunswick, NJ 08901-8521, USA.. kerkof@imcs.rutgers.edu
SO FEMS microbiology letters, **(2000 Mar 1)** 184 (1) 95-101.
Journal code: 7705721. ISSN: 0378-1097.
(Investigators: Garland J, KSC)
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Space Life Sciences
EM 200004
ED Entered STN: 20000505
Last Updated on STN: 20000505
Entered Medline: 20000421
AB In this report, we describe an experiment conducted at Kennedy Space Center in the biomass production chamber (BPC) using soybean plants for purification and processing of human hygiene water. Specifically, we tested whether it was possible to detect changes in the root-associated bacterial assemblage of the plants and ultimately to identify the specific microorganism(s) which differed when plants were exposed to hygiene water and other hydroponic media. Plants were grown in hydroponics media corresponding to four different treatments: control (Hoagland's solution), artificial gray water (Hoagland's+surfactant), filtered gray water collected from human subjects on **site**, and unfiltered gray water. Differences in rhizosphere microbial populations in all experimental treatments were observed when compared to the control treatment using both community level physiological profiles (BIOLOG) and molecular fingerprinting of 16S rRNA genes by terminal **restriction fragment length** polymorphism analysis (TRFLP). Furthermore, screening of a clonal library of 16S rRNA genes by TRFLP yielded nearly full **length** SSU genes associated with the various treatments. Most 16S rRNA genes were affiliated with the Klebsiella, Pseudomonas, Variovorax, Burkholderia, Bordetella and Isosphaera groups. This molecular approach demonstrated the ability to rapidly detect and identify microorganisms unique to experimental treatments and provides a means to fingerprint microbial communities in the biosystems being developed at NASA for optimizing advanced life support operations.

L4 ANSWER 8 OF 83 MEDLINE on STN
AN 2000129296 MEDLINE
DN PubMed ID: 10667834
TI Analysis of point mutation in exon 2 of CYP2E1 gene in renal cell/urothelial cancer patients in comparison with control population.
AU Farker K; Lehmann M H; Kastner R; Weber J; Janitzky V; Schubert J; Hoffmann A
CS Institute of Clinical Pharmacology, Jena, Germany.
SO International journal of clinical pharmacology and therapeutics, **(2000 Jan)** 38 (1) 30-4.
Journal code: 9423309. ISSN: 0946-1965.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200003
ED Entered STN: 20000320
Last Updated on STN: 20000320
Entered Medline: 20000308

AB OBJECTIVE: Genetic polymorphisms of human cytochrome P450s have been implicated to be of importance for susceptibility to different cancers. Recently, a point mutation was found in the exon 2 of the CYP2E1 gene (CYP2E1*2) [Hu et al. 1997]. In order to evaluate a possible link between the point mutation in exon 2 of the CYP2E1 gene and the susceptibility to renal cell/urothelial cancer, we developed a screening method based on the polymerase chain reaction (PCR) and **restriction fragment length** polymorphism (RFLP). MATERIAL: DNA of peripheral white blood cells was isolated from 158 renal cell/urothelial cancer patients as well as from 150 controls. METHOD: Primers for PCR were designed by the Primer 3 release 0.1 **program**. The PCR yield a product of 215 base pairs (bp), which was digested with the restriction enzyme Hha I. The DNA fragments were separated on a 3% agarose gel stained with ethidium bromide. Restriction enzyme digestion of the PCR product obtained from the wild-type DNA resulted in the appearance of a 66 bp, a 43 bp, a 40 bp, a 39 bp and a 28 bp DNA fragment. In contrast to the wild-type, the digestion of the PCR product from DNA carrying the point mutation resulted in the loss of the 39 bp and 40 bp fragments and the appearance of an additional 79 bp fragment. Therefore, the loss of one Hha I restriction **site** caused by a single nucleotide exchange is suitable for the identification of the point mutation in exon 2 of CYP2E1 gene. RESULTS: However, we could not detect any point mutation in any of the 158 renal cell/urothelial cancer patients or the 150 controls. The distribution of the point mutation in exon 2 of CYP2E1 gene did not show any difference in renal cell/urothelial cancer patients and controls. CONCLUSION: This might indicate a lack of association between this CYP2E polymorphism (CYP2E1*2) and renal cell/urothelial cancer.

L4 ANSWER 9 OF 83 MEDLINE on STN
AN 1999450166 MEDLINE
DN PubMed ID: 10520448
TI Bovine ornithine decarboxylase gene: cloning, structure and polymorphisms.
AU Yao J; Zadworny D; Aggrey S E; Kuhnlein U; Hayes J F
CS Dept. of Animal Science, McGill University, Quebec, Canada.
SO DNA sequence : journal of DNA sequencing and mapping, **(1998 Mar)** 8 (4) 203-13.
Journal code: 9107800. ISSN: 1042-5179.
CY Switzerland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U36394
EM 199912
ED Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991202
AB Bovine ornithine decarboxylase (ODC) genomic clones were isolated from a bacteriophage lambda DASH genomic library. A total of 9452 bp **sequence** was determined which covers the entire **sequence** of the bovine ODC gene. **Sequence** analysis showed that the bovine ODC gene consisted of 12 exons which encode a protein identical to that inferred from a bovine ODC cDNA. Comparison of the structure and nucleotide **sequence** of the bovine, human and mouse ODC genes revealed that the gene was highly conserved. Primer extension analysis demonstrated that the transcription start point of bovine ODC mRNA was located 378 bp upstream from the A residue in the translation initiation codon. The 5'-untranslated region (UTR) of ODC mRNA was highly G + C rich, particularly in its 5'-most portion, and **computer** predictions suggested a very stable secondary structure for this region, with an overall free energy of formation of -134.4 kcal/mol. Conserved **sequences** and potential promoter elements including a TATA box, a possible CCAAT element, SP1 ranscription factor binding **sites** (GC boxes) and cAMP response elements (CRE) were identified in the 5'-flanking region of the gene. Two polymorphic restriction **sites**

, a TaqI and a MspI, were mapped to the ODC gene and PCR-based methods for detection of the 2 polymorphisms were developed.

L4 ANSWER 10 OF 83 MEDLINE on STN
AN 1999441476 MEDLINE
DN PubMed ID: 10511805
TI The application of end user computing (EUC) for detection of lipoprotein lipase gene abnormality.
AU Li J; Kobori K; Kondo A; Yonekawa O; Kanno T
CS Department of Laboratory Medicine, Hamamatsu University School of Medicine.
SO Rinsho byori. Japanese journal of clinical pathology, **(1999 Aug)** 47 (8) 737-43.
Journal code: 2984781R. ISSN: 0047-1860.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA Japanese
FS Priority Journals
EM 199910
ED Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991029
AB Lipoprotein lipase (LPL) is an enzyme digesting lipoprotein triglyceride (TG) in peripheral blood vessels. Most patients with LPL deficiency show very high plasma TG and low HDL-C. To establish an effective **computer**-based screening system to identify individuals with genetic LPL disorders, we selected 50 subjects whose plasma TG was over 350mg/dl and HDL-C was lower than 35mg/dl from patients at Hamamatsu University Hospital. We applied End User Computing (EUC) of our laboratory system to select high risk subjects with LPL gene abnormalities. Polymerase chain reaction (PCR) products from LPL gene exons 2-9 were screened by single-strand conformation polymorphism (SSCP), direct DNA **sequence** analysis and **restriction fragment length** polymorphism (RFLP). We found a novel missense mutation (1223C-->G, S323C) in LPL gene exon 7 from three subjects. By PCR-mediated **site**-directed mutagenesis and restriction digestion, the three subjects were found to be heterozygous. In addition, we identified two other common mutations in Japanese employing the RFLP method. One was the 1595C-->G (S447X) in exon 9 from six subjects, two homozygous and four heterozygous individuals. The other was a mutation of intron 3 (C-->T transition) from four heterozygous subjects. Using EUC screening method, we detected genetic LPL abnormalities more easily. The frequency of the LPL gene mutation in the 50 high-risk subjects was 26%, and was estimated to be one out of 2,000 patients at our clinic. Using the EUC system to screen for LPL mutations was established to be an effective **computer**-based screening system to identify individuals with genetic abnormalities.